Soria	CRF Errors Corrected by the STIC Systems British Bridge Black Bridge Bri
	Changed the margins in cases where the sequence text was "wrapped" down to the next line.
	Edited a format error in the Current Application Data section, specifically:
	Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other
	Added the mandatory heading and subheadings for "Current Application Data".
7	Edited the Number of Sequences field. The applicant spelled out a number instead of using an integer.
	Changed the spelling of a mandatory field (the headings or subheadings), specifically:
	Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
	Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited:
	Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
]	Inserted colons after headings/subheadings. Headings edited included:+, .
]	Deleted extra, invalid, headings used by an applicant, specifically:
	Deleted: non-ASCII garbage at the beginning/end of files: secretary initials/filename at end of file page numbers throughout text; other invalid text, such as
]	Inserted mandatory headings, specifically:
]	Corrected an obvious erro: in the response, specifically:
]	Edited identifiers where upper case is used but lower case is required, or vice versa.
	Corrected an error in the Number of Sequences field, specifically:
	A "Hard Pago Break" code was inserted by the applicant. All occurrences had to be deleted.
•	Deloted ending stop codon in amino acid sequences and adjusted the "(A)Length:" lield accordingly (error due to a Patentin bug). Sequences corrected:
	Other:

Action. DO NOT send a copy of this form.

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